

SEQUENCE LISTING

<110> TAKAIWA, MIKIO

OKUDA, MITSUYOSHI

SAEKI, KATSUHISA

KUBOTA, HIROMI

HITOMI, JUN

KAGEYAMA, YASUSHI

SHIKATA, SHITSUW

NOMURA, MASAFUMI

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<141> 2000-04-06

<150> PCT/JP98/04528

<151> 1998-10-07

<150> JP 9-274570

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Ile	Thr	Val	Gly	Ala	Thr	Glu	Asn	Leu	Arg	Pro	Ser	Phe	Gly	Ser	Tyr			
					390					395					400			
gca	gat	aat	att	aac	cac	gtt	gca	cag	ttc	tct	tcc	cgt	ggc	ccg	aca			1248
Ala	Asp	Asn	Ile	Asn	His	Val	Ala	Gln	Phe	Ser	Ser	Arg	Gly	Pro	Thr			
				405				410						415				
aaa	gat	ggg	cga	atc	aag	cct	gat	gtc	atg	gcg	cca	ggg	aca	tac	att			1296
Lys	Asp	Gly	Arg	Ile	Lys	Pro	Asp	Val	Met	Ala	Pro	Gly	Thr	Tyr	Ile			
			420					425					430					
tta	tca	gca	aga	tct	tct	ctt	gca	ccc	gat	tcc	tcc	ttc	tgg	gcg	aat			1344
Leu	Ser	Ala	Arg	Ser	Ser	Leu	Ala	Pro	Asp	Ser	Ser	Phe	Trp	Ala	Asn			
			435				440						445					
cat	gac	agc	aaa	tat	gcc	tat	atg	ggg	gga	acg	tcc	atg	gca	aca	ccg			1392
His	Asp	Ser	Lys	Tyr	Ala	Tyr	Met	Gly	Gly	Thr	Ser	Met	Ala	Thr	Pro			
			450			455				460								
att	gtt	gcg	ggg	aat	gtt	gca	cag	ctc	cgt	gag	cat	ttt	gtg	aaa	aat			1440
Ile	Val	Ala	Gly	Asn	Val	Ala	Gln	Leu	Arg	Glu	His	Phe	Val	Lys	Asn			
					470					475					480			
aga	gga	atc	act	cct	aag	cct	tcc	cta	ttg	aaa	gca	gct	ttg	att	gca			1488
Arg	Gly	Ile	Thr	Pro	Lys	Pro	Ser	Leu	Leu	Lys	Ala	Ala	Leu	Ile	Ala			
				485				490						495				
ggg	gct	gct	gat	gtt	gga	ttg	ggg	tat	ccg	aac	gga	aac	caa	gga	tgg			1536
Gly	Ala	Ala	Asp	Val	Gly	Leu	Gly	Tyr	Pro	Asn	Gly	Asn	Gln	Gly	Trp			
			500					505					510					
ggc	cga	gtg	acc	ctg	gat	aaa	tcg	ttg	aac	gtt	gcc	tat	gtg	aac	gaa			1584
Gly	Arg	Val	Thr	Leu	Asp	Lys	Ser	Leu	Asn	Val	Ala	Tyr	Val	Asn	Glu			
			515				520					525						
tcc	agt	gcc	cta	tca	act	agc	caa	aaa	gcg	aca	tat	acc	ttt	act	gca			1632
Ser	Ser	Ala	Leu	Ser	Thr	Ser	Gln	Lys	Ala	Thr	Tyr	Thr	Phe	Thr	Ala			
			530			535						540						
acg	gcg	ggc	aag	cca	ttg	aaa	atc	tcc	ctg	gta	tgg	tcg	gat	gcc	cct			1680
Thr	Ala	Gly	Lys	Pro	Leu	Lys	Ile	Ser	Leu	Val	Trp	Ser	Asp	Ala	Pro			
					550					555					560			

gca agc act act gct tct gta acc ctg gtc aat gat ttg gat ttg gtc 1728
 Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu Asp Leu Val
 565 570 575

att aca gca cca aac gga aca aga tat gtc ggg aat gac ttc tca gca 1776
 Ile Thr Ala Pro Asn Gly Thr Arg Tyr Val Gly Asn Asp Phe Ser Ala
 580 585 590

cca ttt gac aat aac tgg gat ggc cgc aat aac gta gaa aat gta ttt 1824
 Pro Phe Asp Asn Asn Trp Asp Gly Arg Asn Asn Val Glu Asn Val Phe
 595 600 605

att aat tcg ccc caa agt gga aca tat acc att gag gtg caa gca tat 1872
 Ile Asn Ser Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val Gln Ala Tyr
 610 615 620

aat gtg ccg gtt gga cca caa aac ttc tcg ttg gca att gtg aac taa 1920
 Asn Val Pro Val Gly Pro Gln Asn Phe Ser Leu Ala Ile Val Asn
 625 630 635

<210> 4

<211> 639

<212> PRT

<213> Bacillus sp.

<400> 4

Met Arg Lys Lys Lys Val Phe Leu Ser Val Leu Ser Ala Ala Ala Ile
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Leu Ser Thr Val Ala Leu Asn Asn Pro Ser Ala Gly Asp Ala Arg Thr
 20 25 30

Phe Asp Leu Asp Phe Lys Gly Ile Gln Thr Thr Thr Asp Val Ser Gly
 35 40 45

Phe Ser Lys Gln Arg Gln Thr Gly Ala Ala Ala Phe Leu Val Glu Ser
 50 55 60

Glu Asn Val Lys Leu Leu Lys Gly Leu Leu Lys Lys Leu Glu Thr Val
 65 70 75 80

Pro Ala Asn Asn Lys Leu His Ile Val Gln Phe Asn Gly Pro Ile Leu
 85 90 95

Glu Glu Thr Lys Gln Lys Leu Glu Thr Thr Gly Ala Lys Ile Leu Asp
 100 105 110

Tyr Ile Pro Asp Tyr Ala Tyr Ile Val Glu Tyr Glu Gly Asp Val Gln
115 120 125

Ser Lys Val Arg Ser Ile Glu His Val Glu Ser Val Glu Pro Tyr Leu
130 135 140

Pro Lys Tyr Lys Ile Asp Pro Gln Leu Phe Thr Lys Gly Ala Ser Thr
145 150 155 160

Leu Val Lys Ala Leu Ala Leu Asp Thr Lys Gln Asn Asn Lys Glu Val
165 170 175

Gln Leu Arg Gly Ile Glu Glu Ile Ala Gln Tyr Val Ala Ser Asn Asp
180 185 190

Val His Tyr Ile Thr Ala Lys Pro Glu Tyr Lys Val Met Asn Asp Val
195 200 205

Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser Tyr Gly Leu
210 215 220

Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly Leu Asp Thr
225 230 235 240

Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly Lys Ile Thr
245 250 255

Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp Thr Asn Gly
260 265 270

His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly Ala Thr Asn
275 280 285

Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile Met Asp
290 295 300

Ser Ser Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln Thr Leu Phe
305 310 315 320

Ser Gln Ala Phe Ser Ala Gly Ala Arg Ile His Thr Asn Ser Trp Gly
325 330 335

Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn Val Asp Asp
340 345 350

Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala Gly Asn Glu
355 360 365

Arg Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys Asn Ala
370 375 380

Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe Gly Ser Tyr
385 390 395 400

Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg Gly Pro Thr
405 410 415

Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly Thr Tyr Ile
420 425 430

Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp Ala Asn
435 440 445

His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala Thr Pro
450 455 460

Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Val Lys Asn
465 470 475 480

Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala Leu Ile Ala
485 490 495

Gly Ala Ala Asp Val Gly Leu Gly Tyr Pro Asn Gly Asn Gln Gly Trp
500 505 510

Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr Val Asn Glu
515 520 525

Ser Ser Ala Leu Ser Thr Ser Gln Lys Ala Thr Tyr Thr Phe Thr Ala
530 535 540

Thr Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser Asp Ala Pro
545 550 555 560

Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu Asp Leu Val
565 570 575

Ile Thr Ala Pro Asn Gly Thr Arg Tyr Val Gly Asn Asp Phe Ser Ala
580 585 590

Pro Phe Asp Asn Asn Trp Asp Gly Arg Asn Asn Val Glu Asn Val Phe
 595 600 605

Ile Asn Ser Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val Gln Ala Tyr
 610 615 620

Asn Val Pro Val Gly Pro Gln Asn Phe Ser Leu Ala Ile Val Asn
 625 630 635

<210> 5

<211> 1923

<212> DNA

<213> Bacillus sp.

<220>

<221> CDS

<222> (1)..(1923)

<400> 5

atg	aga	aag	aag	aaa	aag	gtg	ttt	tta	tct	gtt	tta	tca	gct	gca	gcg	48
Met	Arg	Lys	Lys	Lys	Lys	Val	Phe	Leu	Ser	Val	Leu	Ser	Ala	Ala	Ala	
1				5					10					15		

att	ttg	tcg	act	gtt	gcg	tta	agt	aat	cca	tct	gca	ggg	ggg	gca	agg	96
Ile	Leu	Ser	Thr	Val	Ala	Leu	Ser	Asn	Pro	Ser	Ala	Gly	Gly	Ala	Arg	
			20					25					30			

aat	ttt	gat	ctg	gat	ttc	aaa	gga	att	cag	aca	aca	act	gat	gct	aaa	144
Asn	Phe	Asp	Leu	Asp	Phe	Lys	Gly	Ile	Gln	Thr	Thr	Thr	Asp	Ala	Lys	
		35					40					45				

ggg	ttc	tcc	aag	cag	ggg	cag	act	ggg	gct	gct	gct	ttt	ctg	gtg	gaa	192
Gly	Phe	Ser	Lys	Gln	Gly	Gln	Thr	Gly	Ala	Ala	Ala	Phe	Leu	Val	Glu	
	50					55					60					

tct	gaa	aat	gtg	aaa	ctc	cca	aaa	ggg	ttg	cag	aag	aag	ctt	gaa	aca	240
Ser	Glu	Asn	Val	Lys	Leu	Pro	Lys	Gly	Leu	Gln	Lys	Lys	Leu	Glu	Thr	
65					70					75					80	

gtc	ccg	gca	aat	aat	aaa	ctc	cat	att	atc	caa	ttc	aat	gga	cca	att	288
Val	Pro	Ala	Asn	Asn	Lys	Leu	His	Ile	Ile	Gln	Phe	Asn	Gly	Pro	Ile	
				85					90					95		

tta	gaa	gaa	aca	aaa	cag	cag	ctg	gaa	aaa	aca	ggg	gca	aag	att	ctc	336
Leu	Glu	Glu	Thr	Lys	Gln	Gln	Leu	Glu	Lys	Thr	Gly	Ala	Lys	Ile	Leu	
				100					105					110		

jac tac ata cct gat tat gct tac att gtc gag tat gag ggc gat gtt asp Tyr Ile Pro Asp Tyr Ala Tyr Ile Val Glu Tyr Glu Gly Asp Val 115 120 125	384
aag tca gca aca agc acc att gag cac gtg gaa tcc gtg gag cct tat lys Ser Ala Thr Ser Thr Ile Glu His Val Glu Ser Val Glu Pro Tyr 130 135 140	432
ttg ccg ata tac aga ata gat ccc cag ctt ttc aca aaa ggg gca tca Leu Pro Ile Tyr Arg Ile Asp Pro Gln Leu Phe Thr Lys Gly Ala Ser 145 150 155 160	480
gag ctt gta aaa gca gtg gcg ctt gat aca aag cag aaa aat aaa gag Glu Leu Val Lys Ala Val Ala Leu Asp Thr Lys Gln Lys Asn Lys Glu 165 170 175	528
gtg caa tta aga ggc atc gaa caa atc gca caa ttc gca ata agc aat Val Gln Leu Arg Gly Ile Glu Gln Ile Ala Gln Phe Ala Ile Ser Asn 180 185 190	576
gat gtg cta tat att acg gca aag cct gag tat aag gtg atg aat gat Asp Val Leu Tyr Ile Thr Ala Lys Pro Glu Tyr Lys Val Met Asn Asp 195 200 205	624
gtt gcg cgt gga att gtc aaa gcg gat gtg gct cag agc agc tac ggg Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser Tyr Gly 210 215 220	672
ttg tat gga caa gga cag atc gta gcg gtt gcc gat aca ggg ctt gat Leu Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly Leu Asp 225 230 235 240	720
aca ggt cgc aat gac agt tcg atg cat gaa gcc ttc cgc ggg aaa att Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly Lys Ile 245 250 255	768
act gca tta tat gca ttg gga cgg acg aat aat gcc aat gat acg aat Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp Thr Asn 260 265 270	816
ggc cat ggt acg cat gtg gct ggc tcc gta tta gga aac ggc tcc act Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly Ser Thr 275 280 285	864
aat aaa gga atg gcg cct cag gcg aat cta gtc ttc caa tct atc atg Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile Met 290 295 300	912
gat agc ggt ggg gga ctt gga gga cta cct tcg aat ctg caa acc tta Asp Ser Gly Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln Thr Leu 305 310 315 320	960
ttc agc caa gca tac agt gct ggt gcc aga att cat aca aac tcc tgg Phe Ser Gln Ala Tyr Ser Ala Gly Ala Arg Ile His Thr Asn Ser Trp 325 330 335	1008
gga gca gca gtg aat ggg gct tac aca aca gat tcc aga aat gtg gat Gly Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn Val Asp 340 345 350	1056

gac tat gtg cgc aaa aat gat atg acg atc ctt ttc gct gcc ggg aat Asp Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala Gly Asn 355 360 365	1104
gaa gga ccg aac ggc gga acc atc agt gca cca ggc aca gct aaa aat Glu Gly Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys Asn 370 375 380	1152
gca ata aca gtc gga gct acg gaa aac ctc cgc cca agc ttt ggg tct Ala Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe Gly Ser 385 390 395 400	1200
tat gcg gac aat atc aac cat gtg gca cag ttc tct tca cgt gga ccg Tyr Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg Gly Pro 405 410 415	1248
aca aag gat gga cgg atc aaa ccg gat gtc atg gca ccg gga acg ttc Thr Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly Thr Phe 420 425 430	1296
ata cta tca gca aga tct tct ctt gca ccg gat tcc tcc ttc tgg gcg Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp Ala 435 440 445	1344
aac cat gac agt aaa tat gca tac atg ggt gga acg tcc atg gct aca Asn His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala Thr 450 455 460	1392
ccg atc gtt gct gga aac gtg gca cag ctt cgt gag cat ttt gtg aaa Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Val Lys 465 470 475 480	1440
aac aga ggc atc aca cca aag cct tct cta tta aaa gcg gca ctg att Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala Leu Ile 485 490 495	1488
gcc ggt gca gct gac atc ggc ctt ggc tac ccg aac ggt aac caa gga Ala Gly Ala Ala Asp Ile Gly Leu Gly Tyr Pro Asn Gly Asn Gln Gly 500 505 510	1536
tgg gga cga gtg aca ttg gat aaa tcc ctg aac gtt gcc tat gtg aac Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr Val Asn 515 520 525	1584
gag tcc agt tct cta tcc acc agc caa aaa gcg acg tac tcg ttt act Glu Ser Ser Ser Leu Ser Thr Ser Gln Lys Ala Thr Tyr Ser Phe Thr 530 535 540	1632
gct act gcc ggc aag cct ttg aaa atc tcc ctg gta tgg tct gat gcc Ala Thr Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser Asp Ala 545 550 555 560	1680
cct gcg agc aca act gct tcc gta acg ctt gtc aat gat ctg gac ctt Pro Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu Asp Leu 565 570 575	1728
gtc att acc gct cca aat ggc aca cag tat gta gga aat gac ttt act Val Ile Thr Ala Pro Asn Gly Thr Gln Tyr Val Gly Asn Asp Phe Thr 580 585 590	1776

:cg cca tac aat gat aac tgg gat ggc cgc aat aac gta gaa aat gta 1824
 Ser Pro Tyr Asn Asp Asn Trp Asp Gly Arg Asn Asn Val Glu Asn Val
 595 600 605

:tt att aat gca cca caa agc ggg acg tat aca att gag gta cag gct 1872
 Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val Gln Ala
 610 615 620

:at aac gta ccg gtt gga cca cag acc ttc tcg ttg gca att gtg aat 1920
 Tyr Asn Val Pro Val Gly Pro Gln Thr Phe Ser Leu Ala Ile Val Asn
 525 630 635 640

:aa 1923

<210> 6

<211> 640

<212> PRT

<213> Bacillus sp.

<400> 6

Met Arg Lys Lys Lys Lys Val Phe Leu Ser Val Leu Ser Ala Ala Ala
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Ile Leu Ser Thr Val Ala Leu Ser Asn Pro Ser Ala Gly Gly Ala Arg
 20 25 30

Asn Phe Asp Leu Asp Phe Lys Gly Ile Gln Thr Thr Thr Asp Ala Lys
 35 40 45

Gly Phe Ser Lys Gln Gly Gln Thr Gly Ala Ala Ala Phe Leu Val Glu
 50 55 60

Ser Glu Asn Val Lys Leu Pro Lys Gly Leu Gln Lys Lys Leu Glu Thr
 65 70 75 80

Val Pro Ala Asn Asn Lys Leu His Ile Ile Gln Phe Asn Gly Pro Ile
 85 90 95

Leu Glu Glu Thr Lys Gln Gln Leu Glu Lys Thr Gly Ala Lys Ile Leu
 100 105 110

Asp Tyr Ile Pro Asp Tyr Ala Tyr Ile Val Glu Tyr Glu Gly Asp Val
 115 120 125

Lys Ser Ala Thr Ser Thr Ile Glu His Val Glu Ser Val Glu Pro Tyr
 130 135 140

Leu Pro Ile Tyr Arg Ile Asp Pro Gln Leu Phe Thr Lys Gly Ala Ser
 145 150 155 160

Glu Leu Val Lys Ala Val Ala Leu Asp Thr Lys Gln Lys Asn Lys Glu
 165 170 175

Val Gln Leu Arg Gly Ile Glu Gln Ile Ala Gln Phe Ala Ile Ser Asn
 180 185 190

Asp Val Leu Tyr Ile Thr Ala Lys Pro Glu Tyr Lys Val Met Asn Asp
 195 200 205

Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser Tyr Gly
 210 215 220

Leu Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly Leu Asp
 225 230 235 240

Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly Lys Ile
 245 250 255

Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp Thr Asn
 260 265 270

Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly Ser Thr
 275 280 285

Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile Met
 290 295 300

Asp Ser Gly Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln Thr Leu
 305 310 315 320

Phe Ser Gln Ala Tyr Ser Ala Gly Ala Arg Ile His Thr Asn Ser Trp
 325 330 335

Gly Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn Val Asp
 340 345 350

Asp Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala Gly Asn
 355 360 365

Ile Gly Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys Asn
 370 375 380

Ala Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe Gly Ser
 385 390 395 400

Tyr Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg Gly Pro
 405 410 415

Thr Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly Thr Phe
 420 425 430

Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp Ala
 435 440 445

Asn His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala Thr
 450 455 460

Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Val Lys
 465 470 475 480

Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala Leu Ile
 485 490 495

Ala Gly Ala Ala Asp Ile Gly Leu Gly Tyr Pro Asn Gly Asn Gln Gly
 500 505 510

Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr Val Asn
 515 520 525

Glu Ser Ser Ser Leu Ser Thr Ser Gln Lys Ala Thr Tyr Ser Phe Thr
 530 535 540

Ala Thr Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser Asp Ala
 545 550 555 560

Pro Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu Asp Leu
 565 570 575

Val Ile Thr Ala Pro Asn Gly Thr Gln Tyr Val Gly Asn Asp Phe Thr
 580 585 590

Ser Pro Tyr Asn Asp Asn Trp Asp Gly Arg Asn Asn Val Glu Asn Val
 595 600 605

Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val Gln Ala
 610 615 620

Tyr Asn Val Pro Val Gly Pro Gln Thr Phe Ser Leu Ala Ile Val Asn
 625 630 635 640

<210> 7

<211> 1923

<212> DNA

<213> Bacillus sp.

<220>

<221> CDS

<222> (1)..(1923)

<400> 7

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Met	Arg	Lys	Lys	Lys	Lys	Val	Phe	Leu	Ser	Val	Leu	Ser	Ala	Ala	Ala	
1				5					10					15		

att	ttg	tcg	act	gtt	gcg	tta	agt	aat	cca	tct	gca	ggt	ggt	gca	agg	96
Ile	Leu	Ser	Thr	Val	Ala	Leu	Ser	Asn	Pro	Ser	Ala	Gly	Gly	Ala	Arg	
			20					25					30			

aat	ttt	gat	ctg	gat	ttc	aaa	gga	att	cag	aca	aca	act	gat	gct	aaa	144
Asn	Phe	Asp	Leu	Asp	Phe	Lys	Gly	Ile	Gln	Thr	Thr	Thr	Asp	Ala	Lys	
		35					40					45				

ggt	ttc	tcc	aag	cag	ggg	cag	act	ggt	gct	gct	gct	ttt	ctg	gtg	gaa	192
Gly	Phe	Ser	Lys	Gln	Gly	Gln	Thr	Gly	Ala	Ala	Ala	Phe	Leu	Val	Glu	
	50					55					60					

tct	gaa	aat	gtg	aaa	ctc	cca	aaa	ggt	ttg	cag	aag	aag	ctt	gaa	aca	240
Ser	Glu	Asn	Val	Lys	Leu	Pro	Lys	Gly	Leu	Gln	Lys	Lys	Leu	Glu	Thr	
	65				70					75					80	

gtc	ccg	gca	aat	aat	aaa	ctc	cat	att	atc	caa	ttc	aat	gga	cca	att	288
Val	Pro	Ala	Asn	Asn	Lys	Leu	His	Ile	Ile	Gln	Phe	Asn	Gly	Pro	Ile	
				85					90					95		

tta	gaa	gaa	aca	aaa	cag	cag	ctg	gaa	aaa	aca	ggg	gca	aag	att	ctc	336
Leu	Glu	Glu	Thr	Lys	Gln	Gln	Leu	Glu	Lys	Thr	Gly	Ala	Lys	Ile	Leu	
			100					105					110			

gac	tac	ata	cct	gat	tat	gct	tac	att	gtc	gag	tat	gag	ggc	gat	gtt	384
Asp	Tyr	Ile	Pro	Asp	Tyr	Ala	Tyr	Ile	Val	Glu	Tyr	Glu	Gly	Asp	Val	
		115					120					125				

<p> tag tca gca aca agc acc att gag cac gtg gaa tcc gtg gag cct tat ys Ser Ala Thr Ser Thr Ile Glu His Val Glu Ser Val Glu Pro Tyr 130 135 140 </p>	432
<p> tgc ccg ata tac aga ata gat ccc cag ctt ttc aca aaa ggg gca tca leu Pro Ile Tyr Arg Ile Asp Pro Gln Leu Phe Thr Lys Gly Ala Ser 145 150 155 160 </p>	480
<p> gag ctt gta aaa gca gtg gcg ctt gat aca aag cag aaa aat aaa gag flu Leu Val Lys Ala Val Ala Leu Asp Thr Lys Gln Lys Asn Lys Glu 165 170 175 </p>	528
<p> gtg caa tta aga ggc atc gaa caa atc gca caa ttc gca ata agc aat val Gln Leu Arg Gly Ile Glu Gln Ile Ala Gln Phe Ala Ile Ser Asn 180 185 190 </p>	576
<p> gat gtg cta tat att acg gca aag cct gag tat aag gtg atg aat gat asp Val Leu Tyr Ile Thr Ala Lys Pro Glu Tyr Lys Val Met Asn Asp 195 200 205 </p>	624
<p> gtt gcg cgt gga att gtc aaa gcg gat gtg gct cag agc agc tac ggg Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser Tyr Gly 210 215 220 </p>	672
<p> ttg tat gga caa gga cag atc gta gcg gtt gcc gat aca ggg ctt gat Leu Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly Leu Asp 225 230 235 240 </p>	720
<p> aca ggt cgc aat gac agt tcg atg cat gaa gcc ttc cgc ggg aaa att Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly Lys Ile 245 250 255 </p>	768
<p> act gca tta tat gca ttg gga cgg acg aat aat gcc aat gat acg aat Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp Thr Asn 260 265 270 </p>	816
<p> ggt cat ggt acg cat gtg gct ggc tcc gta tta gga aac ggc tcc act Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly Ser Thr 275 280 285 </p>	864
<p> aat aaa gga atg gcg cct cag gcg aat cta gtc ttc caa tct atc atg Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile Met 290 295 300 </p>	912
<p> gat agc ggt ggg gga ctt gga gga cta cct tcg aat ctg caa acc tta Asp Ser Gly Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln Thr Leu 305 310 315 320 </p>	960
<p> ttc agc caa gca tac agt gct ggt gcc aga att cat aca aac tcc tgg Phe Ser Gln Ala Tyr Ser Ala Gly Ala Arg Ile His Thr Asn Ser Trp 325 330 335 </p>	1008
<p> gga gca gca gtg aat ggg gct tac aca aca gat tcc aga aat gtg gat Gly Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn Val Asp 340 345 350 </p>	1056
<p> gac tat gtg cgc aaa aat gat atg acg atc ctt ttc gct gcc ggg aat Asp Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala Gly Asn 355 360 365 </p>	1104

jaa gga ccg aac ggc gga acc atc agt gca cca ggc aca gct aaa aat 3lu Gly Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys Asn 370 375 380	1152
gca ata aca gtc gga gct acg gaa aac ctc cgc cca agc ttt ggg tct Ala Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe Gly Ser 385 390 395 400	1200
tat gcg gac aat atc aac cat gtg gca cag ttc tct tca cgt gga ccg Tyr Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg Gly Pro 405 410 415	1248
aca aag gat gga cgg atc aaa ccg gat gtc atg gca ccg gga acg ttc Thr Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly Thr Phe 420 425 430	1296
ata cta tca gca aga tct tct ctt gca ccg gat tcc tcc ttc tgg gcg Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp Ala 435 440 445	1344
aac cat gac agt aaa tat gca tac atg ggt gga acg tcc atg gct aca Asn His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala Thr 450 455 460	1392
ccg atc gtt gct gga aac gtg gca cag ctt cgt gag cat ttt gtg aaa Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Val Lys 465 470 475 480	1440
aac aga ggc atc aca cca aag cct tct cta tta aaa gcg gca ctg att Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala Leu Ile 485 490 495	1488
gcc ggt gca gct gac atc ggc ctt ggc tac ccg aac ggt aac caa gga Ala Gly Ala Ala Asp Ile Gly Leu Gly Tyr Pro Asn Gly Asn Gln Gly 500 505 510	1536
tgg gga cga gtg aca ttg gat aaa tcc ctg aac gtt gcc tat gtg aac Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr Val Asn 515 520 525	1584
gag tcc agt tct cta tcc acc agc caa aaa gcg acg tac tcg ttt act Glu Ser Ser Ser Leu Ser Thr Ser Gln Lys Ala Thr Tyr Ser Phe Thr 530 535 540	1632
gct act gcc ggc aag cct ttg aaa atc tcc ctg gta tgg tct gat gcc Ala Thr Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser Asp Ala 545 550 555 560	1680
cct gcg agc aca act gct tcc gta acg ctt gtc aat gat ctg gac ctt Pro Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu Asp Leu 565 570 575	1728
gtc att acc gct cca aat ggc aca cag tat gta gga aat gac ttt act Val Ile Thr Ala Pro Asn Gly Thr Gln Tyr Val Gly Asn Asp Phe Thr 580 585 590	1776
tcg cca tac aat gat aac tgg gat ggc cgc aat aac gta gaa aat gta Ser Pro Tyr Asn Asp Asn Trp Asp Gly Arg Asn Asn Val Glu Asn Val 595 600 605	1824

ttt att aat gca cca caa agc ggg acg tat aca att gaa gta cag gct 1872
 phe ile asn ala pro gln ser gly thr tyr thr ile glu val gln ala
 610 615 620

tat aac gta ccg gtt gga cca cag aac ttc tcg ttg gca att gtg aat 1920
 tyr asn val pro val gly pro gln asn phe ser leu ala ile val asn
 625 630 635 640

taa 1923

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<211> 640

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Asn Phe Asp Leu Asp Phe Lys Gly Ile Gln Thr Thr Thr Asp Ala Lys
 35 40 45

Gly Phe Ser Lys Gln Gly Gln Thr Gly Ala Ala Ala Phe Leu Val Glu
 50 55 60

Ser Glu Asn Val Lys Leu Pro Lys Gly Leu Gln Lys Lys Leu Glu Thr
 65 70 75 80

Val Pro Ala Asn Asn Lys Leu His Ile Ile Gln Phe Asn Gly Pro Ile
 85 90 95

Leu Glu Glu Thr Lys Gln Gln Leu Glu Lys Thr Gly Ala Lys Ile Leu
 100 105 110

Asp Tyr Ile Pro Asp Tyr Ala Tyr Ile Val Glu Tyr Glu Gly Asp Val
 115 120 125

Lys Ser Ala Thr Ser Thr Ile Glu His Val Glu Ser Val Glu Pro Tyr
 130 135 140

eu Pro Ile Tyr Arg Ile Asp Pro Gln Leu Phe Thr Lys Gly Ala Ser
 45 150 155 160

Glu Leu Val Lys Ala Val Ala Leu Asp Thr Lys Gln Lys Asn Lys Glu
 165 170 175

Val Gln Leu Arg Gly Ile Glu Gln Ile Ala Gln Phe Ala Ile Ser Asn
 180 185 190

Asp Val Leu Tyr Ile Thr Ala Lys Pro Glu Tyr Lys Val Met Asn Asp
 195 200 205

Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser Tyr Gly
 210 215 220

Leu Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly Leu Asp
 225 230 235 240

Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly Lys Ile
 245 250 255

Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp Thr Asn
 260 265 270

Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly Ser Thr
 275 280 285

Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile Met
 290 295 300

Asp Ser Gly Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln Thr Leu
 305 310 315 320

Phe Ser Gln Ala Tyr Ser Ala Gly Ala Arg Ile His Thr Asn Ser Trp
 325 330 335

Gly Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn Val Asp
 340 345 350

Asp Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala Gly Asn
 355 360 365

Glu Gly Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys Asn
 370 375 380

la Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe Gly Ser
 85 390 395 400

yr Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg Gly Pro
 405 410 415

hr Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly Thr Phe
 420 425 430

le Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp Ala
 435 440 445

sn His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala Thr
 450 455 460

ro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Val Lys
 465 470 475 480

sn Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala Leu Ile
 485 490 495

ala Gly Ala Ala Asp Ile Gly Leu Gly Tyr Pro Asn Gly Asn Gln Gly
 500 505 510

rrp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr Val Asn
 515 520 525

lu Ser Ser Ser Leu Ser Thr Ser Gln Lys Ala Thr Tyr Ser Phe Thr
 530 535 540

ala Thr Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser Asp Ala
 545 550 555 560

Pro Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu Asp Leu
 565 570 575

Val Ile Thr Ala Pro Asn Gly Thr Gln Tyr Val Gly Asn Asp Phe Thr
 580 585 590

Ser Pro Tyr Asn Asp Asn Trp Asp Gly Arg Asn Asn Val Glu Asn Val
 595 600 605

Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val Gln Ala
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Tyr Asn Val Pro Val Gly Pro Gln Asn Phe Ser Leu Ala Ile Val Asn
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Tyr Gly Leu Tyr
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<210> 10
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 <212> PRT
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<400> 10

Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser Tyr Gly Leu
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<210> 11
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<400> 11

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<210> 12
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 <212> PRT
 <213> Bacillus sp.

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Ser Tyr Ala Asp
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<210> 13

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<212> PRT

<213> Bacillus sp.

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23

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23

210> 21

211> 21

212> DNA

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220>

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211> 21

212> DNA

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21

<210> 23

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:210> 24

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:23> Description of Artificial Sequence: primer

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21